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EXAMINER
SCHLAPKOHL, WALTER

ART UNIT	PAPER NUMBER
1636	

SHORTENED STATUTORY PERIOD OF RESPONSE	NOTIFICATION DATE	DELIVERY MODE
3 MONTHS	04/13/2007	ELECTRONIC

Please find below and/or attached an Office communication concerning this application or proceeding.

If NO period for reply is specified above, the maximum statutory period will apply and will expire 6 MONTHS from the mailing date of this communication.

Notice of this Office communication was sent electronically on the above-indicated "Notification Date" and has a shortened statutory period for reply of 3 MONTHS from 04/13/2007.

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Office Action Summary	Application No.	Applicant(s)	
	10/524,619	JANE ET AL.	
	Examiner	Art Unit	
	Walter Schlapkohl	1636	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *12/4/2006*.

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1-7,12 and 16* is/are pending in the application.

4a) Of the above claim(s) *7,12 and 16* is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *1-6* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☒ The drawing(s) filed on *09 February 2005* is/are: a)☐ accepted or b)☒ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☒ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☒ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☒ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☒ Information Disclosure Statement(s) (PTO/SB/08) Paper No(s)/Mail Date *8/23/06, 1/5/06, 1/9/06*.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____.
5) ☐ Notice of Informal Patent Application
6) ☒ Other: *Exhibits A and B*.

DETAILED ACTION

Receipt is acknowledged of the papers filed 12/4/2006 in which claims 7, 12 and 16 were amended, and claims 8-11, 13-15 and 17-21 were cancelled. Claims 1-7, 12 and 16 are pending. Claims 7, 12 and 16 are withdrawn. Claims 1-6 are under examination in the instant Office action.

Election/Restrictions

Applicant's election of Group I (claims 1-6) in the reply filed on 12/4/2006 is acknowledged. Because Applicant did not distinctly and specifically point out the supposed errors in the restriction requirement, the election has been treated as an election without traverse (MPEP § 818.03(a)).

Priority

Applicant's claim for the benefit of a prior-filed application under 35 U.S.C. 119(e) or under 35 U.S.C. 120, 121, or 365(c) is acknowledged. Applicant has not complied with one or more conditions for receiving the benefit of an earlier filing date under 35 U.S.C. 119(e) as follows:

The later-filed application must be an application for a patent for an invention which is also disclosed in the prior

application (the parent or original nonprovisional application or provisional application). The disclosure of the invention in the parent application and in the later-filed application must be sufficient to comply with the requirements of the first paragraph of 35 U.S.C. 112. See *Transco Products, Inc. v. Performance Contracting, Inc.*, 38 F.3d 551, 32 USPQ2d 1077 (Fed. Cir. 1994).

The disclosure of the prior-filed application, Application No. 60/402,055, fails to provide adequate support or enablement in the manner provided by the first paragraph of 35 U.S.C. 112 for one or more claims of this application. Specifically, Application No. 60/402,055 does not provide support for "[a]n isolated nucleic acid molecule comprising a sequence of nucleotides encoding or complementary to a sequence encoding a mammalian transcription factor comprising an amino acid sequence having at least 75% identity to SEQ ID NO:8 (human SOM) or SEQ ID NO:16 (murine SOM) after optimal alignment" (claim 1). The prior-filed application appears only to have support for ranges which specify at least about 75% similarity. The same appears to be true for the foreign priority document, Australia 2002951579. Similarly, the disclosure of the prior filed applications fail to provide support or enablement in the manner provided by the first paragraph of 35 U.S.C. 112 for claim 2,

wherein claim 2 recites high stringency conditions which are (0.1X SSC, 0.1% w/v SDS at 65°C). Therefore, for claims 1 and 2 Applicant has been granted priority only to the date of filing of the PCT application of which the instant Application is the national stage version: 8/8/2003.

Sequence Compliance

This application contains sequence disclosures that are encompassed by the definitions for nucleotide and/or amino acid sequences set forth in 37 CFR 1.821(a)(1) and (a)(2). However, this application fails to comply with the requirements of 37 CFR 1.821 through 1.825 because sequences are set forth in the drawings that lack sequence identifiers (see, e.g., Figures 1A, 1C and 3A). It is often convenient to identify sequences in figures by amending the Brief Description of the Drawings section (see MPEP 244.02). If the sequences are already present in the sequence listing, it would be remedial to amend the Brief Description of the Drawings to include the appropriate sequence identifiers. Applicants are required to comply with all of the requirements of 37 CFR 1.821 - 1.825. Any response to this office action that fails to meet all of these requirements will be considered non-responsive. The nature of the noncompliance with the requirements of 37 C.F. R. 1.821 through 1.825 did not

preclude the examination of the application on the merits, the results of which are communicated below.

Drawings

The drawings are objected to under 37 CFR 1.83(a) because they fail to show Figures 5E and 5F as described in the specification. Furthermore, the specification fails to include a figure description for Figures 7E and 7F. Any structural detail that is essential for a proper understanding of the disclosed invention should be shown in the drawing. MPEP § 608.02(d). Corrected drawing sheets in compliance with 37 CFR 1.121(d) are required in reply to the Office action to avoid abandonment of the application. Any amended replacement drawing sheet should include all of the figures appearing on the immediate prior version of the sheet, even if only one figure is being amended. The figure or figure number of an amended drawing should not be labeled as "amended." If a drawing figure is to be canceled, the appropriate figure must be removed from the replacement sheet, and where necessary, the remaining figures must be renumbered and appropriate changes made to the brief description of the several views of the drawings for consistency. Additional replacement sheets may be necessary to show the renumbering of the remaining figures. Each drawing

sheet submitted after the filing date of an application must be labeled in the top margin as either "Replacement Sheet" or "New Sheet" pursuant to 37 CFR 1.121(d). If the changes are not accepted by the examiner, the applicant will be notified and informed of any required corrective action in the next Office action. The objection to the drawings will not be held in abeyance.

Claim Rejections - 35 USC § 112

The following is a quotation of the second paragraph of 35 U.S.C. 112:

> The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

Claims 1-2, and therefore dependent claims 3-6, are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which Applicant regards as the invention.

Claim 1 recites "[a]n isolated nucleic acid molecule comprising a sequence of nucleotides encoding or complementary to a sequence encoding a mammalian transcription factor comprising an amino acid sequence having at least 75% identity to SEQ ID NO:8 (human SOM) or SEQ ID NO:16 (murine SOM) after

optimal alignment" in lines 1-4 (emphasis added). Claim 1 is vague and indefinite in that the metes and bounds of "optimal alignment" are unclear. Does Applicant intend an alignment comprising the highest percentage of homology possible, or does Applicant intend some other form of "optimal" alignment.

Claim 1 is also vague and indefinite in that it is unclear whether Applicant intends to claim an isolated nucleic acid limited to one encoding or complementary to a sequence encoding a mammalian transcription factor comprising an amino acid sequence having at least 75% identity to *SEQ ID NO:8* or to *human SOM* (or, similarly, to SEQ ID NO:16 or to murine SOM). A broad range or limitation together with a narrow range or limitation that falls within the broad range or limitation (in the same claim) is considered indefinite, since the resulting claim does not clearly set forth the metes and bounds of the patent protection desired. See MPEP § 2173.05(c). Note the explanation given by the Board of Patent Appeals and Interferences in *Ex parte Wu*, 10 USPQ2d 2031, 2033 (Bd. Pat. App. & Inter. 1989), as to where broad language is followed by "such as" and then narrow language. The Board stated that this can render a claim indefinite by raising a question or doubt as to whether the feature introduced by such language is (a) merely exemplary of the remainder of the claim, and therefore not

required, or (b) a required feature of the claims. Note also, for example, the decisions of *Ex parte Steigewald*, 131 USPQ 74 (Bd. App. 1961); *Ex parte Hall*, 83 USPQ 38 (Bd. App. 1948); and *Ex parte Hasche*, 86 USPQ 481 (Bd. App. 1949). In the present instance, claim 1 recites the broad recitation human SOM (which includes allelic variants, mutants, etc.), and the claim also recites SEQ ID NO:8 which is the narrower embodiment of the range/limitation.

Claim 2 recites "[t]he isolated nucleic acid molecule of claim 1 wherein the molecule has a nucleotide sequence selected from the group consisting of: SEQ ID NO: 7 (human *som*), SEQ ID NO:15 (murine *som*), and a nucleotide sequence capable of hybridizing to SEQ ID NO: 7, SEQ ID NO:15 or a complementary form of any of the foregoing under high stringency conditions (0.1X SSC, 0.1% w/v SDS at 65°C)" in lines 1-5 (emphasis added). Claim 2 is vague and indefinite in that the metes and bounds of "high stringency conditions" are unclear. Does Applicant intend to limit the scope of the claims to hybridization conditions which are "0.1X SSC, 0.1% w/v SDS at 65°C" or does Applicant intend to include other embodiments of high stringency conditions as presented in the specification, e.g., "from at least about 31% v/v to at least about 50% v/v formamide and from at least about 0.01 M to at least about 0.15 M salt for

hybridization, and at least about 0.01 M to at least about 0.15 M salt for washing conditions" (see page 24, lines 1-4). As explained above, a broad range or limitation together with a narrow range or limitation that falls within the broad range or limitation (in the same claim) is considered indefinite, since the resulting claim does not clearly set forth the metes and bounds of the patent protection desired. See MPEP § 2173.05(c).

Claim 2 is also vague and indefinite in that the metes and bounds of a "complementary form" of a nucleic acid which is capable of hybridizing to SEQ ID NO:7 or SEQ ID NO:15 are unclear. Does Applicant intend complementary forms which are complementary by two or more nucleotides, or does Applicant intend only nucleic acids which are capable of hybridizing to the complement of SEQ ID NO:7 or SEQ ID NO:15?

The following is a quotation of the first paragraph of 35 U.S.C. 112:

> The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

Claim 2 is rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the written description requirement.

The claims contain subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventors, at the time the application was filed, had possession of the claimed invention. **This is a new matter rejection.**

The specification as originally filed does not provide support for the invention as now claimed: "...high stringency conditions (0.1X SSC, 0.1% w/v SDS at 65°C)." The specification does not provide sufficient blazemarks nor direction for the instant hybridization conditions encompassed by the above-mentioned limitation, as currently recited because the specification recites high stringency conditions wherein the conditions can include 0.1X SSC, 0.1% w/v SDS at a temperature of at least 65°C. The instant claims now recite a limitation, which was not clearly disclosed in the specification as filed, and now changes the scope of the instant disclosure as filed. Such a limitation recited in the present claims, which did not appear in the specification as filed, introduces new concepts and violates the description requirement of the first paragraph of 35 U.S.C. 112.

The following is a quotation of the first paragraph of 35 U.S.C. 112:

> The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

Claims 1-2 are rejected under 35 U.S.C. 112, first paragraph, because the specification, while being enabling for an isolated nucleic acid encoding SEQ ID NO:8 or SEQ ID NO:16, does not reasonably provide enablement for a nucleic acid encoding or complementary to a mammalian transcription factor (i.e., any MGH homolog) comprising any polypeptide with at least 75% identity to SEQ ID NO:8 or SEQ ID NO:16. The specification does not enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to use the invention commensurate in scope with these claims.

The factors considered when determining if the disclosure satisfies the enablement requirement and whether any necessary experimentation is undue include, but are not limited to: 1) nature of the invention, 2) state of the prior art, 3) relative skill of those in the art, 4) level of predictability in the art, 5) existence of working examples, 6) breadth of claims, 7) amount of direction or guidance by the inventor, and 8) quantity

of experimentation needed to make or use the invention. *In re Wands*, 858 F.2d 731, 737, 8 USPQ2d 1400, 1404 (Fed. Cir. 1988).

The claims are drawn to a nucleic acid encoding or complementary to any MGH homolog comprising any polypeptide with at least 75% identity to SEQ ID NO:8 or SEQ ID NO:16, both referred to as SOM. Because the nucleic acid sequence can be any complement of any nucleic acid encoding an MGH homolog, there is in essence no functional limitation in the claims. Applicant has taught the polypeptides consisting of SEQ ID NO:8 and SEQ ID NO:15. A knockout mouse model of the murine *som* gene was shown to have neural tube defects (p. 78, Example 16). The specification does not teach a working example of a SOM polypeptide or a nucleic acid encoding a SOM polypeptide wherein the polypeptide functions as a transcription factor. Based on the guidance provided by the specification, the nucleic acids function is based entirely on the homology of the polypeptide(s) encoded therefrom.

The claim encompasses an unreasonable number of inoperative nucleic acids/ polypeptides, which the skilled artisan would not know how to use. While the specification teaches that the polypeptide of SEQ ID NO:8 or SEQ ID NO:16 is a transcription factor homolog of mammalian *grainyhead*, this teaching is predicated 100% on the homology these sequences have in

comparison to other *grainyhead* transcription factors. As opposed to the claims, what is disclosed about SOM is narrow: two nucleic acids which encode a polypeptide with one disclosed function and no other obvious specific functions. The prior art does teach a nucleic acid encoding a polypeptide of SEQ ID NO:8 which can heterodimerize with MGR and Brother-of-MGR, but not with more distant members of the *grainyhead* family (Ting et al, *Biochem. J.* **370**:953-962, 2003; IDS Ref.; see entire document, especially page 953, the Abstract and pages 95-959, Figure 3), but the prior art does not recognize properties of the polypeptide except as a *grainyhead* family member with transactivation, DNA-binding and dimerization domains capable of binding two other *grainyhead* family transcription factors. And while the skill in the transcription factor art is high, the genes which are regulated by either human or murine SOM are unknown. Furthermore, Ting et al also teach that SOM comes in three isoforms, one of which lacks a transactivation domain and which, as a result, may have a repressor function opposite to the other two isoforms (see e.g., page 961, paragraph bridging 1st and 2nd columns). Therefore, the state of the art with respect to SOM transcription factors is underdeveloped.

There are no working examples of nucleic acid sequences which encode transcription factors with less than 100% identity

to the polypeptides SEQ ID NO:8 or SEQ ID NO: 16. The only function attributed to SOM is as a transcription factor but this function has not been confirmed with functional assays. The skilled artisan would not know how to use any nucleic acid which encodes or is complementary to a nucleic acid which encodes a polypeptides with 75% identity of SEQ ID NO:8 or SEQ ID NO:16 on the basis of teachings in the prior art or specification. Furthermore, it is acknowledged that transcription factors even within the *grainyhead* family display highly divergent tissue-specific expression and roles in development. (Wilanowski, et al. *Mechanisms in Development* **114**:37-50, 2002; IDS Ref.; see entire document, especially page 37, the Abstract and page 46, 1st column, 1st full paragraph). The specification does not provide guidance for using nucleic acids encoding polypeptides related to (*i.e.*, 75%-99% identity) but not identical those encoded by SEQ ID NO:7 and SEQ ID NO: 15. The specification does teach that SOM comprises a DNA-binding domain and a dimerization domain which are highly conserved in *grainyhead* family members (see Table 4 on page 69). However, the specification does not teach which domains outside these domains are characteristic of a SOM polypeptide or a SOM polypeptides specific function. The claims are broad because they do not require the claimed nucleic acid to be encode a polypeptide to

be identical to the disclosed sequences and because the claims have no functional limitation due to the inclusion of sequences which are simply complementary to nucleic acids which encode MGH homologs with 75% identity to human or murine SOM.

For these reasons, which include the complexity and unpredictability of the nature of the invention and art in terms of the diversity of *grainyhead* transcription factors and lack of knowledge about function(s) of encompassed nucleic acids which encode polypeptides structurally related to SEQ ID NO:8 and SEQ ID NO:16, the limited examples of nucleic acids encoding SOM polypeptides and their function, the lack of direction or guidance for using polypeptides that are not identical to SEQ ID NO:8 or SEQ ID NO:16, and the breadth of the claims for structure without function, it would require undue experimentation to use the invention commensurate in scope with the claims.

Applicant is reminded that *Vas-Cath* makes clear that the written description provision of 35 U.S.C. §112 is severable from its enablement provision (see page 1115).

Claims 1-2 are rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the written description requirement. The claim(s) contains subject matter which was not

described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

The claims are drawn to nucleic acids encoding or complementary to a sequence encoding a mammalian transcription factor comprising an amino acid sequence having at least 75% identity to human SOM or to murine SOM after optimal alignment. Claim 2 is further limited to such nucleic acid molecules selected from SEQ ID NO:7, SEQ ID NO:15 and nucleotide sequences capable of hybridizing to SEQ ID NO:7, SEQ ID NO:15 or a complementary form of any of the foregoing under stringency conditions. The claims thus encompass any nucleic acid sequence which is complementary to a sequence encoding a mammalian transcription factor (defined in the specification as "a homolog of *Drosophila grh*, i.e. M-GRH" see page 5, lines 3-4) comprising human or murine SOM-encoding sequences. Because the specification has defined complementary as "the capacity for precise pairing between two nucleobases of an oligomeric compound" (see page 59, lines 25-26), the claims encompass any nucleic acid sequence comprising at least two "nucleobases" which can precisely pair with any sequence present in a nucleic acid which encodes a homolog of M-GRH comprising an amino acid

sequence having at least 75% identity to human or murine *som* after optimal alignment. Because two nucleotides complementary to, e.g., a sequence encoding SEQ ID NO:8 would represent not even a single percent of identity (2/1821 nucleotides (minimum) would be 0.1% identity), the claims encompass at least nucleotides sequences with as little as 0.1% identity to, e.g., SEQ ID NO:7). The encompassed sequences need not encode a transcription factor at all.

To provide adequate written description and evidence of possession of a claimed genus, the specification must provide sufficient distinguishing identifying characteristics of the genus. The factors to be considered include disclosure of a complete or partial structure, physical and/or chemical properties, functional characteristics, structure/function correlation, and any combination thereof. The specification describes human and murine nucleic acid sequences which encode human and murine SOM, respectively (see, e.g. Examples 8-9 at pages 73-74 and SEQ ID NOs: 7 and 15). These molecules belong to a family of transcriptions factors which are homologs of *grainyhead*, a transcription factor present in *Dropshophila melanogaster* (see, e.g., Table 2 at pages 9-11). The specification further teaches that the full length human SOM showed ">60% similarity" at the protein level with other

existing MGF family members (see page 73, lines 11-14). Other than a GRLH-3 mutant designed for knockout SOM expression in mice, no description is provided of a single mutant SOM sequence or of a single polymorphism or variant of either human or murine SOM.

Even if one accepts that the examples described in the specification meet the claim limitations of the rejected claims with regard to structure and function, the examples are only representative of two nucleic acid sequences which encode or are complementary to a sequence which encodes homologs of M-GRH and/or which are capable of hybridizing to SEQ ID NO:7, 15 or complementary forms thereof. Thus, it is impossible to extrapolate from the examples described herein those nucleic acid molecules that would necessarily meet the structural/functional characteristics of the rejected claims, i.e., which of the encompassed nucleic acids are SOMs, especially in comparison to other homologs of M-GRH.

The prior art does not appear to offset the deficiencies of the instant specification in that it does not describe a set of genes which encode proteins that have at least 75% identity to any human SOM or any murine SOM. Ting et al teach that the Drosophila gene *grainyhead* is the founding member of a large family of genes encoding developmental transcription factors

that are highly conserved from fly to human (*Biochem. J.* **370**:953-962, 2003; IDS Ref.; see entire document, especially page 953, the Abstract). Ting et al further teach a nucleic acid encoding a SOM polypeptide of SEQ ID NO:8 which can heterodimerize with MGR and Brother-of-MGR, but not with more distant members of the *grainyhead*; see entire document, especially page 953, the Abstract and pages 95-959, Figure 3). However, the prior art does not recognize properties of the polypeptide except as a *grainyhead* family member with transactivation, DNA-binding and dimerization domains which is capable of binding two other *grainyhead* family transcription factors. Furthermore, Ting et al also teach that SOM comes in three isoforms, one of which lacks a transactivation domain and which, as a result, may have a repressor function opposite to the other two isoforms (see e.g., page 961, paragraph bridging 1st and 2nd columns). Moreover, it is acknowledged that transcription factors even within the *grainyhead* family display highly divergent tissue-specific expression and roles in development. (Wilanowski, et al. *Mechanisms in Development* **114**:37-50, 2002; IDS Ref.; see entire document, especially page 37, the Abstract and page 46, 1st column, 1st full paragraph).

Thus, given the lack of knowledge with regard to sequences related to nucleic acids which encode or are complementary to

nucleic acids which encode polypeptides with 75% identity to human or murine SOM, and given the large family of related transcription factors with such divergent functions and unrelated expression patterns, one or ordinary skill in the art would not known which related sequences were SOM sequences and which were unrelated *grainyhead* family members. Furthermore, given the very large genus of nucleic acid molecules encompassed by the rejected claims, and given the limited description provided by the prior art and specification with regard to the sequences capable of fulfilling the claim limitations of claims 1-2, the skilled artisan would not have been able to describe the broadly claimed genus of nucleic sequences that a complementary to or encode polypeptides with 75% identity to human or murine SOM. Thus, there is no structural/functional basis provided by the prior art or instant specification for one of skill in the art to envision those nucleic acid sequences that satisfy the "functional limitations" of the claims. Therefore, the skilled artisan would have reasonably concluded Applicant was not in possession of the claimed invention for claims 1-2.

Claim Rejections - 35 USC § 102

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

> A person shall be entitled to a patent unless -
>
> (a) the invention was known or used by others in this country, or patented or described in a printed publication in this or a foreign country, before the invention thereof by the applicant for a patent.
>
> (b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

Claims 1-2 are rejected under 35 U.S.C. 102(a) as being anticipated by Ting et al (*Biochem J.* **370**:953-962, 2003; IDS Ref #2) as evidenced by AY231160 and accompanying sequence alignment (Exhibit A).

Ting et al teach the identification and characterization of human SOM as well as the isolation and identification or murine SOM (see entire document, especially the Abstract; page 1st column, 1st and 2nd full paragraphs; and page 955, 1st column, 2nd full paragraph). Ting et al further teach the nucleic acid encoding human SOM, i.e., SEQ ID NO:7 as evidenced by AY231160. The alignment of SEQ ID NO:7 and that of the disclosed human *som* have been provided as Exhibit A for Applicant's convenience.

Claims 1-2 are rejected under 35 U.S.C. 102(b) as being anticipated by BM460207 (1999).

Note: The claims are drawn to nucleic acids encoding or complementary to a sequence encoding a mammalian transcription factor (defined in the specification as "a homolog of *Drosophila grh*, i.e. M-GRH" --see page 5, lines 3-4) comprising an amino acid sequence having at least 75% identity to human SOM or to murine SOM after optimal alignment. Claim 2 is further limited to such nucleic acid molecules selected from SEQ ID NO:7, SEQ ID NO:15 and nucleotide sequences capable of hybridizing to SEQ ID NO:7, SEQ ID NO:15 or a complementary form of any of the foregoing under "high" stringency conditions. Examiner has interpreted a "complementary form" to include any level of complementarity. The claims thus encompass any nucleic acid sequence which is complementary to *a* sequence encoding an M-GHR homolog comprising human or murine SOM-encoding sequences. Furthermore, because the specification has defined complementary as "the capacity for precise pairing between two nucleobases of an oligomeric compound" (see page 59, lines 25-26), the claims encompass any nucleic acid sequence comprising at least two "nucleobases" which can precisely pair with any sequence present in a nucleic acid which encodes a homolog of M-GRH comprising an amino acid sequence having at least 75% identity to human or

murine *som* after optimal alignment. Because two nucleotides complementary to, e.g., a sequence encoding SEQ ID NO:8 (e.g. SEQ ID NO:7) would represent not even a single percent of identity (2/1870 nucleotides would be 0.1% identity), the claims encompass nucleotide sequences with as little as 0.1% identity to, e.g., SEQ ID NO:7. As claimed, the encompassed sequences need not encode a transcription factor at all.

The sequence disclosed as GenBank Accession No. BM260207 comprises a nucleic acid sequence which is 26.2% identical to SEQ ID NO:7 as indicated by the alignment provided for Applicant as "Exhibit B." Therefore, BM260207 anticipates claims 1-2.

Conclusion

No claim is allowed.

Certain papers related to this application may be submitted to the Art Unit 1636 by facsimile transmission. The faxing of such papers must conform with the notices published in the Official Gazette, 1156 OG 61 (November 16, 1993) and 1157 OG 94 (December 28, 1993) (see 37 C.F.R. § 1.6(d)). The official fax telephone number for the Group is (571) 273-8300. Note: If Applicant *does* submit a paper by fax, the original signed copy should be retained by Applicant or Applicant's representative.

NO DUPLICATE COPIES SHOULD BE SUBMITTED so as to avoid the processing of duplicate papers in the Office.

Any inquiry of a general nature or relating to the status of this application or proceeding should be directed to (571) 272-0547.

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Any inquiry concerning rejections or objections in this communication or earlier communications from the examiner should be directed to Walter Schlapkohl whose telephone number is (571) 272-4439. The examiner can normally be reached on Monday through Friday from 8:30 AM to 5:00 PM.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Dr. Joseph Woitach can be reached at (571) 272-0739.

Walter A. Schlapkohl, Ph.D.
Patent Examiner
Art Unit 1636

March 30, 2007

NANCY VOGEL
PRIMARY EXAMINER

Exhibit A

<!--StartFragment-->ALIGNMENTS

RESULT 1
AY231160
LOCUS AY231160 1870 bp mRNA linear PRI 27-MAR-2003
DEFINITION Homo sapiens sister-of-mammalian grainyhead isoform 1 (SOM) mRNA, complete cds.
ACCESSION AY231160
VERSION AY231160.1 GI:29293714
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1870)
AUTHORS Ting,S.B., Wilanowski,T., Cerruti,L., Zhao,L.L., Cunningham,J.M. and Jane,S.M.
TITLE The identification and characterization of human Sister-of-Mammalian Grainyhead (SOM) expands the grainyhead-like family of developmental transcription factors
JOURNAL Biochem. J. 370 (Pt 3), 953-962 (2003)
PUBMED 12549979
REFERENCE 2 (bases 1 to 1870)
AUTHORS Ting,S.B.
TITLE Direct Submission
JOURNAL Submitted (05-FEB-2003) Bone Marrow Research Laboratories, Royal Melbourne Hospital, Royal Pde., Parkville, VIC 3050, Australia
FEATURES Location/Qualifiers
source 1. .1870
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ORIGIN

Query Match 100.0%; Score 1869.2; DB 5; Length 1870;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 1870; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Exhibit B

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DEFINITION AGENCOURT_6420341 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:5502632 5', mRNA sequence.
ACCESSION BM460207
VERSION BM460207.1 GI:18509247
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1057)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12141 row: b column: 09
High quality sequence stop: 590.
FEATURES Location/Qualifiers
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ORIGIN

Query Match 26.2%; Score 489.8; DB 3; Length 1057;
Best Local Similarity 95.0%; Pred. No. 2e-123;
Matches 514; Conservative 2; Mismatches 24; Indels 1; Gaps 1;

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Qy        587 C 587
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Db        704 C 704
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